

WO 00/04168

SEQUENCE LISTING

Sub A1

- <110> Cahoon, Rebecca E.
Gutteridge, Steven
Lee, Jian Ming
Rafalski, Antoni
- <120> Ornithine Biosynthesis Enzymes
- <130> BB-1174
- <140>
- <141>
- <150> 60/093,209
- <151> July 17, 1998
- <160> 12
- <170> Microsoft Office 97
- <210> 1
- <211> 1201
- <212> DNA
- <213> Zea mays

A

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cacggctgcg ccgtctcctt cgtcggctgc cgctgcacc gcgtcgctga gtcgagtga 240
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cgcccttgca caagggtgt acaccgcaag tatcattgat gggcgtgttc cacaactctc 1020
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atgccttcat ggtattttcc tgtgcctctt ttctcatatt gttgtgtttt atggctatgt 1140
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a 1201

- <210> 2
- <211> 345
- <212> PRT
- <213> Zea mays

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Met Leu Leu Thr Lys Pro Tyr Leu Ser Asn Ser Leu Leu Pro Val Pro
1 5 10 15
Ser Pro Pro Pro Ser Gly Pro Thr Leu Ser Ser Asn His Ala Ser Pro
20 25 30

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Leu Ala Ala Pro Thr Cys Arg Arg Ser Arg Leu Arg Ile Ser Ala Thr
 35 40 45
 Ser Thr Ala Ala Pro Ser Pro Ser Ser Ala Ala Ala Thr Ala Ser
 50 55 60
 Leu Ser Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg
 65 70 75 80
 Phe Lys Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys
 85 90 95
 Ser Pro Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser
 100 105 110
 Cys Val Gly Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile
 115 120 125
 Asn Ser Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asp Gly
 130 135 140
 Leu Arg Val Thr Asp Ala Leu Thr Met Glu Val Val Glu Met Val Leu
 145 150 155 160
 Val Gly Lys Val Asn Lys Asn Leu Val Ser Leu Ile Asn Ile Ala Gly
 165 170 175
 Gly Thr Ala Ile Gly Leu Cys Gly Lys Asp Ala Arg Leu Ile Thr Ala
 180 185 190
 Arg Pro Ser Pro Asn Ala Ala Ala Leu Gly Phe Val Gly Glu Val Ser
 195 200 205
 Arg Val Asp Ala Thr Val Leu His Pro Ile Ile Ala Ala Gly His Ile
 210 215 220
 Pro Val Ile Ala Thr Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn
 225 230 235 240
 Ile Asn Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala
 245 250 255
 Glu Lys Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg
 260 265 270
 Asn Asp Pro Gly Ser Leu Val Lys Val Val Asp Ile Ala Gly Val Arg
 275 280 285
 Lys Met Val Ala Asp Gly Lys Val Ala Gly Gly Met Ile Pro Lys Val
 290 295 300
 Glu Cys Cys Val His Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile
 305 310 315 320
 Ile Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp
 325 330 335
 Glu Gly Thr Gly Thr Met Ile Thr Gly
 340 345

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<210> 3
 <211> 1186
 <212> DNA
 <213> Oryza sativa

<400> 3
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 catcgccgcc tctcccgccc ctcgacgctg cctccgtctc gccgtcacat ccgcccgggc 180
 gccggctgct tcgtccgccc agcgccgggc ggcgtgagc cgcgtggatg tgcctcaga 240
 ggcgctcccc ttcatccagc gcttcaaggg gaagaccgtg gtggtgaagt acggcggcgc 300
 ggcatgaag tcgcccagc tccaggcttc agtgatccgc gacctggctc tctctcgtg 360
 cgtcggcctc caccctgtgc tcgtccacgg cggcgggccc gagatcaact cctggctgct 420
 ccgcgtcggc gtcgagccgc agttccggaa cggcctccgc gtcactgacg cgtcaacat 480
 ggaggtcgtc gagatcgtgc tcgtccgcaa ggtcaacaaa gaactcctct cctcatcaa 540
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 gccctccccg aangaaaagg gcttcgggtt tgcggcggg gtctggcgcg tggacgccac 660
 cgtcctccac ccaatccatg cctccgggtc catcccggtc atcgccactg tggcgccga 720
 cgagaccggg caggccatca acatcaacgc tgacacggcg gccggcgaga tcgcccggc 780
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 gggcgtgcac actgcaagca tcatcgatgg gcgtgtccc cactcgttgc tgcctgagat 1020
 tctcacagat gagggcactg gcactatgat cactggctga ggtgattcat ccgctcgtg 1080
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<210> 4
 <211> 343
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (195)

<400> 4
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 Thr Arg Val Ser Ser Pro Ala Pro Gly Pro Asn His Ala Lys Pro Ile
 20 25 30
 Ala Ala Ser Pro Ala Pro Arg Arg Cys Leu Arg Leu Ala Val Thr Ser
 35 40 45
 Ala Ala Ala Pro Ala Ala Ser Ser Ala Glu Ala Ala Ala Ala Leu Ser
 50 55 60
 Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys
 65 70 75 80
 Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro
 85 90 95
 Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val
 100 105 110

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Gly Leu His Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser
 115 120 125
 Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asn Gly Leu Arg
 130 135 140
 Val Thr Asp Ala Leu Asn Met Glu Val Val Glu Met Val Leu Val Arg
 145 150 155 160
 Lys Val Asn Lys Glu Leu Leu Ser Leu Ile Lys Leu Pro Gly Gly Ser
 165 170 175
 Ala Val Ser Leu Cys Trp Lys Glu Ala Arg Leu Leu Asn Glu Arg Pro
 180 185 190
 Ser Pro Xaa Glu Lys Gly Leu Arg Phe Val Gly Gly Val Trp Arg Val
 195 200 205
 Asp Ala Thr Val Leu His Pro Ile Ile Ala Ser Gly His Ile Pro Val
 210 215 220
 Ile Ala Thr Val Gly Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn
 225 230 235 240
 Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Val Gly Ala Glu Lys
 245 250 255
 Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp
 260 265 270
 Pro Gly Ser Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met
 275 280 285
 Val Ala Asp Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys
 290 295 300
 Cys Val Arg Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp
 305 310 315 320
 Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly
 325 330 335
 Thr Gly Thr Met Ile Thr Gly
 340

<210> 5
 <211> 1204
 <212> DNA
 <213> Glycine max

<400> 5
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 ccaccgcgcc atttccgagg tggcgaacgc ggcgcaacct ccactcgccg ccgccactgc 180
 caccgagggt cagtaccgag tcgatgtgct ctcgagatcg ctccccttca ccagaaaatt 240
 ccgcggcaaa accatcgctg tcaagtacgg cggcgccgcc atgaagtccc cggagctcca 300
 ggctccgctg atcaacgacc ttgtcctcct ctctcgctgc ggctccgcc ccgtcctggt 360
 ccacggcggc ggcccgaga tcaactcctg gctcggcgcg ctcaacatcc ccgccgtctt 420
 ccgcgacggc ctccggtca ccgacgccga caccatggag atcgtctcca tggctcctgt 480
 cggaaaagtc aacaaaaccc tagtttctct aattaacaag gccggcgcca ccgccgtcgg 540

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cctctctggc atggacggcc gcctccctac cgcgcgcgcg gctcccaagg ccgcccagcct 600
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cagccacatc cccgtcgtca cctccgcgcg cgcgcgatgaa tccggacagc ctacaacat 720
caacgccgac accgtcgcgc gagaattggc agcgtcgcgc ggcgcggaga agctgattct 780
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cttgagttga ggttgacatt cagcacttgt tttgttagag attggtgatt ttttttaagt 1140
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<210> 6
 <211> 342
 <212> PRT
 <213> Glycine max

<400> 6
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 Pro Phe Pro Thr Lys Pro Gln Asn Gln Leu Thr Thr Ser His Ala Phe
 20 25 30
 Pro Ser Thr Arg Leu Arg His Arg Ala Ile Ser Ala Val Ala Asn Ala
 35 40 45
 Ala Gln Pro Pro Leu Ala Ala Ala Thr Ala Thr Glu Gly Gln Tyr Arg
 50 55 60
 Val Asp Val Leu Ser Glu Ser Leu Pro Phe Ile Gln Lys Phe Arg Gly
 65 70 75 80
 Lys Thr Ile Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu
 85 90 95
 Leu Gln Ala Ser Val Ile Asn Asp Leu Val Leu Leu Ser Cys Val Gly
 100 105 110
 Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp
 115 120 125
 Leu Gly Arg Leu Asn Ile Pro Ala Val Phe Arg Asp Gly Leu Arg Val
 130 135 140
 Thr Asp Ala Asp Thr Met Glu Ile Val Ser Met Val Leu Val Gly Lys
 145 150 155 160
 Val Asn Lys Thr Leu Val Ser Leu Ile Asn Lys Ala Gly Ala Thr Ala
 165 170 175
 Val Gly Leu Ser Gly Met Asp Gly Arg Leu Leu Thr Ala Arg Pro Ala
 180 185 190
 Pro Lys Ala Ala Asp Leu Gly Tyr Val Gly Gln Val Ala Arg Val Asp
 195 200 205
 Pro Ala Val Leu Arg Ser Leu Ile Asp Thr Ser His Ile Pro Val Val
 210 215 220

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Thr Ser Val Ala Ala Asp Glu Ser Gly Gln Pro Tyr Asn Ile Asn Ala
225 230 235 240

Asp Thr Val Ala Gly Glu Leu Ala Ala Ser Leu Gly Ala Glu Lys Leu
245 250 255

Ile Leu Leu Thr Asp Val Ala Gly Ile Leu Glu Asp Arg Asn Asp Pro
260 265 270

Asp Ser Leu Val Lys Lys Ile Asp Ile Lys Gly Val Lys Lys Met Met
275 280 285

Glu Asp Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Asn Cys Cys
290 295 300

Val Arg Ser Leu Ala Gln Gly Val Ile Thr Ala Ser Ile Ile Asp Gly
305 310 315 320

Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Ala
325 330 335

Gly Thr Met Ile Thr Gly
340

<210> 7
<211> 1246
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (492)..(542)

<400> 7
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ctaacctaaa ggccgcccgc gtcaggcccc tcgctcctc cgcgcccat ggacgccgcg 180
ggctccgcgt ctccgctcc tctcctccc tggcgccagc gcaggccgcg tccgcggcgc 240
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gcgaggtcac gagaaaaaac ccctctgtgc tccaccgat catcgctcc agccacatcc 720
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<210> 8
<211> 340

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<212> PRT

<213> Triticum aestivum

<220>

<221> UNSURE

<222> (133)

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<221> UNSURE

<222> (144)..(160)

<400> 8

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Leu Pro Asn Pro Asn Leu Lys Ala Ala Arg Val Arg Pro Leu Ala Ser
20 25 30

Ser Ala Pro His Gly Arg Arg Gly Leu Arg Val Ser Ala Ser Ser Ser
35 40 45

Ser Leu Ala Pro Ala Gln Ala Ala Ser Ala Ala Leu Asn Arg Val Asp
50 55 60

Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys Gly Lys Thr
65 70 75 80

Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu Leu Gln
85 90 95

Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val Gly Leu Arg
100 105 110

Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp Leu Gln
115 120 125

Arg Val Gly Val Xaa Pro Gln Phe Arg Asn Gly Leu Arg Val Thr Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Lys Gln Leu Leu Ser Leu Ile Arg Pro Ala Gly Thr Thr Ala Val Gly
165 170 175

Leu Cys Arg Lys Asp Gly Arg Ile Leu Thr Glu Arg Pro Ser Pro Asp
180 185 190

Ala Ala Ala Leu Gly Phe Val Gly Glu Val Thr Arg Lys Asn Pro Ser
195 200 205

Val Leu His Pro Ile Ile Ala Ser Ser His Ile Pro Val Ile Ala Thr
210 215 220

Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn Ala Asp Thr
225 230 235 240

Ala Ala Gly Glu Ile Ala Ala Ala Ile Gly Ala Glu Lys Leu Leu Leu
245 250 255

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PCT/US99/15931

Ile Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asp Asp Pro Gly Ser
 260 265 270

Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Arg Met Val Ala Glu
 275 280 285

Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Gly Cys Cys Val Arg
 290 295 300

Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
 305 310 315 320

Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
 325 330 335

Met Ile Thr Gly
 340

<210> 9
 <211> 439
 <212> DNA
 <213> Triticum aestivum

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 ggggtgcggc agatggtatc cgggtgggcag gttgctggtg gaatgatccc aaaggtggag 180
 tgctgcgtga gagccctcgc ccagggtgtg cacactgcaa gcatcatcga tgggcgtgtc 240
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 taaggtgtaa aatgcctcct tggtaacttc ttatgccttt ctgttcatac tgccaatctg 360
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 aaaaaaaaaa aaaaaaaaaa 439

<210> 10
 <211> 100
 <212> PRT
 <213> Triticum aestivum

<400> 10
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Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp Pro Gly Ser
 20 25 30

Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met Val Ser Gly
 35 40 45

Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys Cys Val Arg
 50 55 60

Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
 65 70 75 80

Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
 85 90 95

Met Ile Thr Gly
 100

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<210> 11
 <211> 297
 <212> PRT
 <213> Synechocystis sp.

<400> 11

Met Ser Ser Thr Gln Asp Tyr Ile Gly Glu Glu Ala Ala Thr Arg Val
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Lys Ile Leu Ser Glu Ala Leu Pro Tyr Ile Gln His Phe Ala Gly Arg
 20 25 30

Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Asp Ser Asn Leu
 35 40 45

Lys Asp Lys Val Ile Arg Asp Ile Val Phe Met Ala Ser Val Gly Ile
 50 55 60

Arg Pro Val Val Val His Gly Gly Gly Pro Glu Ile Asn Thr Trp Leu
 65 70 75 80

Asp Lys Val Gly Ile Glu Pro Gln Phe Lys Asp Gly Leu Arg Val Thr
 85 90 95

Asp Ala Ala Thr Met Asp Ile Val Glu Met Val Leu Val Gly Arg Val
 100 105 110

Asn Lys Glu Leu Val Asn Leu Ile Asn Gln Ala Gly Gly Lys Ala Val
 115 120 125

Gly Leu Cys Gly Lys Asp Gly Gln Leu Met Thr Ala Arg Thr Met Thr
 130 135 140

Asn Lys Asp Val Gly Phe Val Gly Glu Val Ser Ser Val Asp Ala Arg
 145 150 155 160

Val Val Glu Thr Leu Val Lys Ser Gly Tyr Ile Pro Val Ile Ser Ser
 165 170 175

Val Ala Ala Asp Glu Phe Gly Gln Ala His Asn Ile Asn Ala Asp Thr
 180 185 190

Cys Ala Gly Glu Leu Ala Ala Ala Leu Gly Ala Glu Lys Leu Ile Leu
 195 200 205

Leu Thr Asp Thr Arg Gly Ile Leu Arg Asp Tyr Lys Asp Pro Ser Thr
 210 215 220

Leu Ile His Lys Leu Asp Ile Gln Gln Ala Arg Glu Leu Ile Gly Ser
 225 230 235 240

Gly Ile Val Ala Gly Gly Met Ile Pro Lys Val Thr Cys Cys Val Arg
 245 250 255

Ser Leu Ala Gln Gly Val Arg Ala Ala His Ile Leu Asp Gly Arg Leu
 260 265 270

Pro His Ala Leu Leu Leu Glu Val Phe Thr Asp Leu Gly Ile Gly Ser
 275 280 285

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PCT/US99/15931

Met Ile Val Ala Ser Gly Tyr Asp Leu
 290 295

<210> 12
 <211> 345
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CONSENSUS

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 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Arg Val Asp Val Leu Ser Glu Xaa Leu Pro Phe Ile Gln Xaa
 65 70 75 80
 Phe Xaa Gly Lys Thr Xaa Val Val Lys Tyr Gly Gly Ala Ala Met Lys
 85 90 95
 Ser Pro Glu Leu Gln Ala Ser Val Ile Xaa Asp Leu Val Leu Leu Ser
 100 105 110
 Cys Val Gly Leu Xaa Pro Val Leu Val His Gly Gly Gly Pro Glu Ile
 115 120 125
 Asn Ser Trp Leu Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Phe Arg Xaa Gly
 130 135 140
 Leu Arg Val Thr Asp Ala Xaa Xaa Met Glu Xaa Val Xaa Met Val Leu
 145 150 155 160
 Val Xaa Lys Val Asn Lys Xaa Leu Xaa Ser Leu Ile Xaa Xaa Xaa Gly
 165 170 175
 Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa
 180 185 190
 Arg Pro Xaa Pro Xaa Xaa Xaa Xaa Leu Xaa Xaa Val Gly Xaa Val Xaa
 195 200 205
 Arg Xaa Xaa Xaa Xaa Val Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa His Ile
 210 215 220
 Pro Val Xaa Xaa Xaa Val Xaa Ala Asp Glu Xaa Gly Gln Xaa Tyr Asn
 225 230 235 240
 Ile Asn Ala Asp Thr Xaa Ala Gly Glu Xaa Ala Ala Xaa Xaa Gly Ala
 245 250 255

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Glu Lys Leu Xaa Leu Xaa Thr Asp Val Xaa Gly Ile Leu Xaa Asp Arg
 260 265 270
 Xaa Asp Pro Xaa Ser Leu Val Lys Xaa Xaa Asp Ile Xaa Gly Val Arg
 275 280 285
 Xaa Met Xaa Xaa Xaa Gly Xaa Val Xaa Gly Gly Met Ile Pro Lys Val
 290 295 300
 Xaa Cys Cys Val Xaa Xaa Leu Ala Gln Gly Val Xaa Thr Ala Ser Ile
 305 310 315 320
 Leu Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp
 325 330 335
 Glu Gly Xaa Gly Thr Met Ile Thr Gly
 340 345

Sub A1
cont.